In the Specification:

Please amend pages 37-38 of the specifiction as follows:

Table 5. Sandwich hybridization probe matrix showing the combination and position of probes, and the signal output at 450 and 655nm.

Probe Combination	Target Species[b]	Probe Positions 5' end[a]	OD@450nm ±SD	OD@655nm ±SD
Het1.25aS (SEQ ID NO: 15)/Raphid1F (SEQ ID NO:8)	*H.akashiwo*	149 / 79	1.595 ±0.209	0.768 ±0.091
Het1.25aS (SEQ ID NO: 15)/Raphid2F (SEQ ID NO:9)	*H.akashiwo*	149 / 344	0.0633 ±0.006	0.058 ±0.003
Het1.25aS (SEQ ID NO: 15)/Het.sig2-3'F (SEQ ID NO:7)	*H.akashiwo*	149 / 366	0.0773 ±0.006	0.063 ±0.002
Het1.25bS (SEQ ID NO: 16)/Raphid1F (SEQ ID NO:8)	*H.akashiwo*	157 / 79	0.583 ±0.081	0.307 ±0.040
Het1.25bS (SEQ ID NO: 16)/Raphid2F (SEQ ID NO:9)	*H.akashiwo*	157 / 344	0.094 ±0.048	0.073 ±0.024
Het1.25bS (SEQ ID NO: 16)/Het.sig2-3'F (SEQ ID NO:7)	*H.akashiwo*	157 / 366	0.054 ±0.003	0.054 ±0.002
Het3S (SEQ ID NO: 17)/Raphid1F (SEQ ID NO:8)	*H.akashiwo*	567 / 79	0.093 ±0.009	0.068 ±0.003
Het3S (SEQ ID NO: 17)/Raphid2F (SEQ ID NO:9)	*H.akashiwo*	567 / 344	0.222 ±0.011	0.128 ±0.002
Het3S (SEQ ID NO: 17)/Het.sig2-3'F (SEQ ID NO:7)	*H.akashiwo*	567 / 366	0.080 ±0.016	0.080 ±0.016
Fib1.25aS (SEQ ID NO: 21)/Raphid1F (SEQ ID NO:8)	*F.japonica*	122 / 49	1.32 ±0.040	0.634 ±0.020

Fib1.25aS (SEQ ID NO: 21)/Raphid2F (SEQ ID NO:9)	*F.japonica*	122 / 322	0.094 ±0.009	0.067 ±0.004
Fib1.25aS (SEQ ID NO: 21)/Fib.sig2-3'F (SEQ ID NO:14)	*F.japonica*	122 / 344	0.087 ±0.006	0.067 ±0.004

[a]Ribosomal RNA complement. Aligned position with respect to target sequence.

[b]The clones used for this analysis are CAWR05 FOR *Heterosigma akashiwo* and CAWRO3 for *Fibrocapsa japonica*. Refer to Table 1 for details about these clones.

The best combinations of probes for signal production in *Heterosigma akashiwo* and *Fibrocapsa japonica* were the Het1.25a capture probe (SEQ ID NO:15)/Raphid1F signal probe (SEQ ID NO:8) and Fib1.25a capture probe (SEQ ID NO:21)/Raphid1F signal probe (SEQ ID NO:8) respectively. These combinations of probes were used in all the following analyses.

Also, the S.H.A. probes were modified from the F.I.S.H. probes due to the higher Tm requirement and this may affect the signal output and specificity. A probe matrix was used to test all possible combinations of capture and signal probes for signal production. The best combination of probes for *Heterosigma akashiwo* and *Fibrocapsa japonica* were then tested for specificity in the S.H.A. format. Figure 1 shows specificity and isolate comparison for the sandwich hybridization assay combinations targeted at *H. akashiwo* and *F. japonica*. A). The probe combination Het1.25aS (SEQ ID NO:15)/Raphid1F (SEQ ID NO:8) which is targeted at *H. akashiwo* was screened against a number of *H. akashiwo* isolates and other raphidophyte species. *H. akashiwo* 1 represents the isolate *H. akashiwo* CAWR04; *H. akashiwo* 2 = CAWR05; *H. akashiwo* 3 = CAWR09 and *H. akashiwo* 4 = CAWR14. The *F. japonica* isolate was CAWR02. B). The probe combination Fib1.25aS/Raphid1F which is targetted at *F. japonica* was screened against two *F. japonica* isolates and other raphidophyte species. *F. japonica* 1 represents the isolate CAWR02 and *F. japonica* 2 represents the isolate CAWR03. The *H. akashiwo* isolate was CAWR05.

Example 8

Standard Curve Construction

The standard curves were constructed by spiking cells which were in log phase growth into 1 L of either filtered sea water (FSW) or field sample, then collecting the cells by gentle filtration and lysing as described above. The concentrated stock solutions were then serially diluted with either lysis/hybridization buffer for the FSW sample or field background for the field